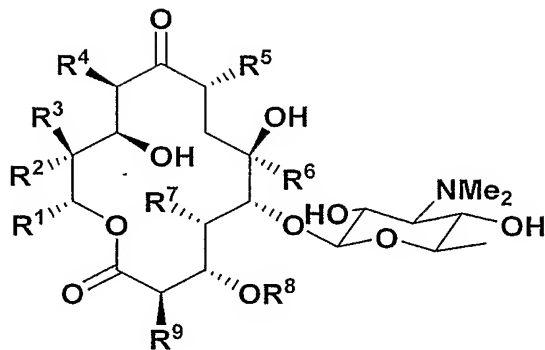
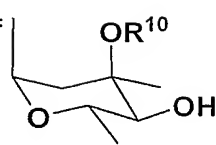


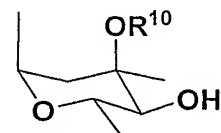
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**Figure 1A**

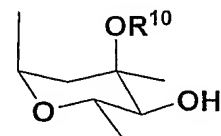
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin B

R<sup>1</sup> = C<sub>2</sub>H<sub>5</sub>    R<sup>2</sup> = R<sup>4</sup> = R<sup>5</sup> = R<sup>6</sup> = R<sup>7</sup> = R<sup>9</sup> = -CH<sub>3</sub>    R<sup>3</sup> = -H    R<sup>8</sup> =

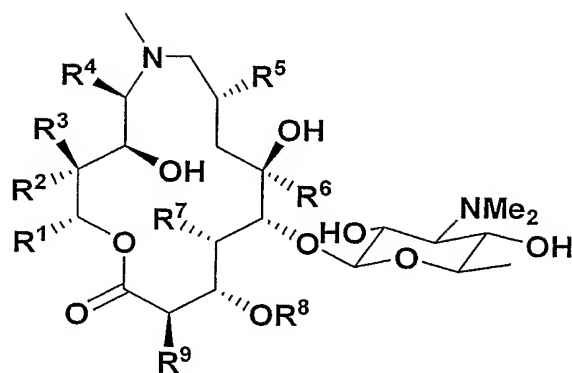
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin A

R<sup>1</sup> = C<sub>2</sub>H<sub>5</sub>    R<sup>2</sup> = R<sup>4</sup> = R<sup>5</sup> = R<sup>6</sup> = R<sup>7</sup> = R<sup>9</sup> = -CH<sub>3</sub>    R<sup>3</sup> = -OH    R<sup>8</sup> =

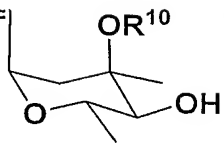
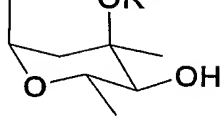
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin C

R<sup>1</sup> = C<sub>2</sub>H<sub>5</sub>    R<sup>2</sup> = R<sup>4</sup> = R<sup>5</sup> = R<sup>6</sup> = R<sup>7</sup> = R<sup>9</sup> = -CH<sub>3</sub>    R<sup>3</sup> = -OH    R<sup>8</sup> =

2/23

**Figure 1B**

5-O-dedesosaminyl-5-O-mycaminosyl-azithromycin

$R^1 = C_2H_5$      $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$      $R^3 = -OH$      $R^8 =$ 

 $OR^{10}$      $R^{10} =$ 


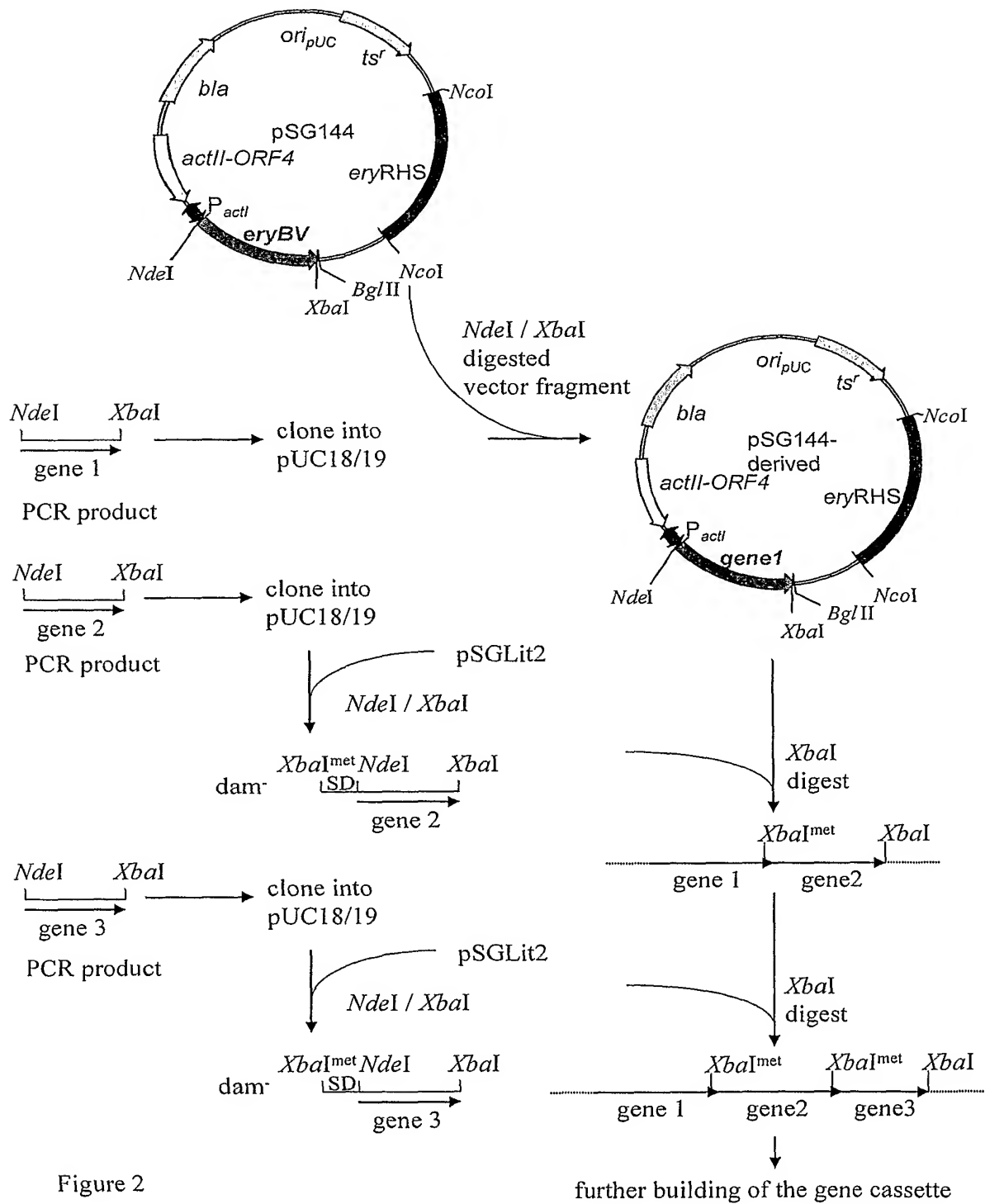
**Figure 2**

Figure 2

### Figure 3

TylA1.pep x u08223.em\_pro2

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5
1 MNDRPRRAMKGII LAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
  |||
1 MNDRPRRAMKGII LAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
10
51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
  |||
51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
15
101 GARHIGGDAAALILGDNVFGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
  |||
101 GARHIGGDAAALILGDNVFGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
20
151 YGVGEIDSGGRLLSLEEKPRRPRSNLAVTGLYLYTNDVVEIARTISPSAR 200
  |||
151 YGVGEIDSGGRLLSLEEKPRRPLEP.GRHRLYLYTNDVVEIARTISPSAR 199
25
201 GELEITDVNKVYLEQGRARLTELGRGFAWLDMGTHDSLLOAGQYVQLLEQ 250
  |||
200 GELEITDVNKVYLEQGRA.AHGAGAVVAWLDMGTHDSLLOAGQYVQLLEQ 248
30
251 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 300
  |||
249 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 298
301 DSRAQ 305
  |||
299 DSRAQ 303

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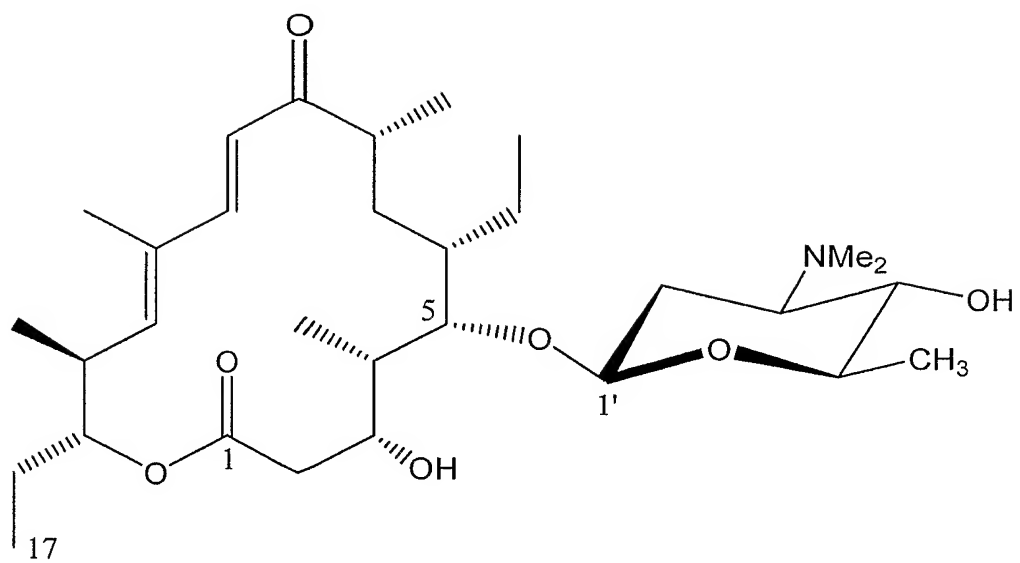
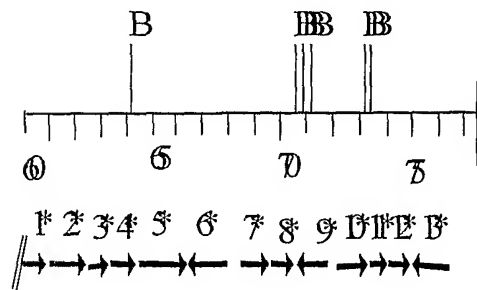
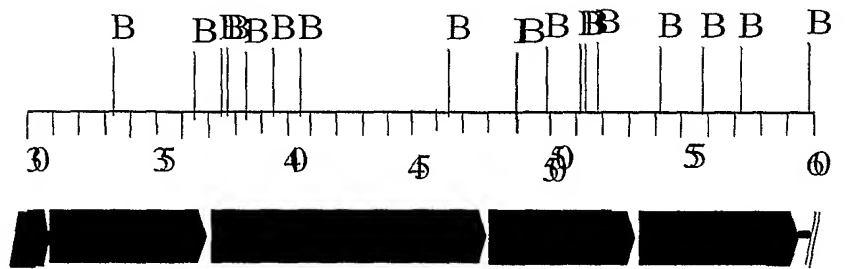
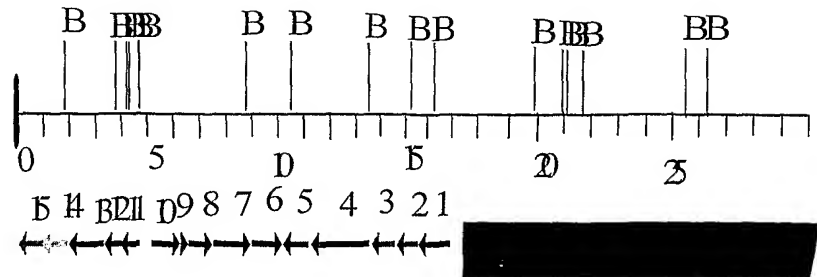
**Figure 5**

Figure 6



**Figure 7**

5           1   GGCATGCCTT CGGGGTGTGC GCGGCGCCT CAGAGCGTGG CCAGTACCTC  
          51   GTGCAGGGCC GCGATCACCT TGTCTGTAC GTCGGGCGCG AGCCCCGGGT  
10       101   ACATCGGCAG CGAGAAGATC TCGTCCGCCA GCCGCTCCGT CACCGGCAGC  
         151   GAGCCCTTGG CGTACCCAG GTGCGCGAAG CCCGTCATGG TGTGCACGGG  
         201   CCACGGGTAA CTGATGTTGA GCGAGATCCC GTACGACTTG AGCGCCTCGA  
15       251   TGATGTCGTC CCGGCGCGGG TGGCGGACGA CGTACACGTA ATACACGTGG  
         301   TCGTTGCCCT CGGTGACGGA CGGCAGCACC AGGCCGCCGG GGCCCGTCAG  
         351   GTTTCGCGAGT CCTTCGGCGT AACGCCGGGC GACCGCGCGC CGGCCCTCGA  
20       401   TGTAGCGGTC GAGGCGGGTG AGCTTGCGGC GCAGGATCTC CGCCTGCACC  
         451   TCGTGAGACC GGCTGTTGTG GCCGGGCGTC TGCACGACGT AGTACACGTC  
25       501   CTCCATGCCG TAGTAGCGCA GCCGGCGCAG CGCACGGTCG ACGTCCGCGT  
         551   CGTCGGTCAG CACGGCCCCG CCGTCGCCGT ACGCACCGAG GACCTTCGTC  
         601   GGGTAGAACG AGAAGGCGGC GGCCTCGCCC AGCGTGCCGG CCAGCTCGCC  
30       651   GTGGTGGCGG GCACCGTGCG CCTGGGCGCA GTCCTCCAGC ACCACCAGGC  
         701   CGTGCTGCTC GGCCAGGGCG CGCAAGGGCG CCATGTCGAC GCACTGCCCCG  
35       751   TACAGGTGCA CCGGCAGCAG GGCCTTCGTG CGCGGGGTGA TGACGTCCGC  
         801   GACCTGGTCG GTGTCCATGA GGTGGTCCTC GGC GCGGACG TCGACGAAGA  
         851   CGGGCGTGGC ACCGGTGCCG TCGATGGCCA CCACCGTCGG CGCGGCCGTG  
40       901   TTGGAGACGG TGACGACCTC GTCCCCGGG CCCACCCCGA GCGCCTGCAG  
         951   ACCCAGCTTG ACGGCGTTGG TGCCGTTGTC GACACGCCG CAGTGGCGCA  
45       1001   GGCCGTGGTA GTCCGGAAC TCCTTCTCGA ACCCGTCCAC GCTGGGGCCG  
         1051   AGGACCAACT GCCCGGAGGC GAAGACGGTC TCGACGGCGT CGAGGAGGTC  
         1101   CGCGCGTTCG TTCTGGTATT CCGCCAGGTA GTCCCAGACG TAGGTAGTCA  
50       1151   CGGAGAGCTC AACCTCCAGA GTGTTTCGAT GGGGTGGTGG GAAGCCGGTG  
         1201   CGCGCGGACC AGGTCGTGCC AGCAGTCGCG GACCGACTCC CGCAGCGAAC  
55       1251   GGCGCGGTGC CCAGCCCAGC AGGGCGCGCG CCGCGCCGGT GTCGACCCGC  
         1301   AGCCAGTCCT CCCGGTGCCC GGGAGCCCGG CCCGGAGCCG GCGCTCCAC  
         1351   CACCCGCGCC GGAATGCCGC TCGCTCGAT GAACAGGCCG ACCAGGTCGC  
60       1401   GGACGGCGAC CGCCTCGCCC CGCCCGATGC CGACGGCGAC CGGGACGGCC



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5 1451 GGTGCGCGGG CGGCGGCCAC GACGGCGTCG GCCACGTCCC GCACATCGAC  
1501 GTAGTCCCGG TGC GCGCGCA GCCGGGACAG TTCCACGACG GCCTCCGCAC  
1551 CCGTCCCGGC GGCCGCCAGC AGCCGCTCGG CGACCTGGCC CAGCAGACTG  
10 1601 ATCCGCGGGG TGCCGGGGCC CGACACGTTG GACACCCGTA GCACCACACC  
1651 GTCGACCCAC CCGCCCGAGG TGCCCCGCAG CACCGCCTCG CTGGCGGCGA  
1701 GCTTGCTCCT GCCGTACGCC GTGTCCGGGC GCGGTACGGC GTCGGCGCCC  
15 1751 ACCGAACCGC CGGGCGTCAC CGGGCCGTAC TCCAGTACCG AGCCGAGGTG  
1801 GACCAGCCGC GGCCGCGCGG ACATCAGCGC CAGCGCCTCC AGCAGGCGCA  
1851 GCGTGGGCAC CGCGGTGGCG GACCACATCT GTCGTCGGT ACGGCCCCAG  
20 1901 ATGCTTCCGA CGGAGTTGAC GATCGTGTCC GGACGCTCCG CGTCCAGGGC  
1951 GGCGGCCAGC GCCGCGGGAT CCGTACCGGC CAGGTCCAGG GTGACGCAGC  
25 2001 GGTACGGCAT CGGCTCCTCG GGCGGGCGGC GGCCACAC CACCACGTCA  
2051 CGGCCCCGCG CGGCGAACGC CGCGCACACA TGCCGGCCGA CGTACCCGGC  
2101 GCCGCCAGG ACCACGACGC TGCCACTGCC ACTGCCGCGC GGCATCGGAT  
30 2151 CGTTCACCAT

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**Figure 8**

5 11301 CGTCAGTACA GCGTGTGGGC ACACGCCACC AGGGTGCGCA GCTCGATGTT  
 11351 GAGGTAGTTG CCGTGCGCCA GCAGCCCGGT GAGCTGACCG AGCGACAGCC  
 11401 AGGCGAAGTC GTCCGGTGCG TCCTCCGGGA AGTCGTGCGG GACCTCCACG  
 10 11451 ATCACGTAGC GGTTCCTGGGC GTGGAAGAAG CGCCCGCCCT CCTCGGACTG  
 11501 GACGGCGTCG TAGCGCACGT CCTGAGGCGG CGCGGACAGC ACGTCCTCCA  
 15 11551 GGTACGGCGG GCCGGGCAGC CCCCGCGGAC CGGTGTGCTC CTGTGGCCGG  
 11601 CACTGGACCG TGGGGGCCAG CTCGGCGACG TTCAGGTGCC CGACGTCCAC  
 11651 CCGTGCCCGC ACGAGCGCGT GCAGCACGCC GTCGACGGAC TTGACCAGCA  
 20 11701 GCGCCATCAG ACCCGGCAGC CGCGGCTCGA TGAGCGGCTG CGTCCAGGAG  
 11751 GTGACCTCCC GGCTGCTGGC GCTGACCTCG GCGGCCATGA CCCGGAAGTG  
 25 11801 CCGCCCGCTC TCGTGGGCGA TCTCGTGCGG CGTGCGGTAC CAGCCGTCCG  
 11851 CCGTCACCGT ATCGAGCGGC ACCCGGTTCT GCACCAGCTC CCGCAGGGCG  
 11901 CGCACACCCG TGAACCACGT CAGGACCTCG GCCGTCTGTG GCCGCGCCGC  
 30 11951 ACCCGGCGAG CCGAAGAAGG AGCGCAGCAC GGGGGACGGG GCGGACGCGT  
 12001 CGGCGTCCGC CGTGGGCAGG CAGGCGAGGA TGGACCGGGC GTCCATGTTG  
 35 12051 ACCACGTTGT CCAGCATCAG CAGCCGGCGG AGCTGCCCCA GCGTCAGCCA  
 12101 GCGGAAGTCC TCCCCGATGT CGAGGTCGTC GTCCGCCGCC AACTCGACGA  
 12151 TCATGTTCCG GTTGCCTTTG GCCAGGACC AGTCCGCCTG TTCGGACTGG  
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 45 12301 CCTGCACGGT CGGCGACACC TGAAGAACGT TGACGTTCCC GGGCTCCATC  
 12351 TTGGCCTGCA TCAGGAAGTG CAGCACCCCG TCGATCTCCC GCGCCACGAT  
 12401 CCCGAGCAGC CCCACCTCCG GCTGCACGAT GATGGGCTGC GTCCAGCCCC  
 50 12451 GCTCGGGCAG CCGGTCCGTA CGGACGTGCA GCCCTCCAC GGAGAAGAAA  
 12501 CGGCCCCGACG CGTGGTGCAG GTTTCCCGTA CCCGGGTGGA AGCTCCAGCC  
 55 12551 GCGCAGCTCC GCGAAGGGAA CGCGGGACAC GTCGAAGCGC CCCGCCCCGA  
 12601 GGCGTTCGGC CAGCCAGCCG GAGATGCCGT CGAACGGCGT GACCGCACTG  
 12651 TCCGCGGTGC GTGCCGACAC CAGCACCCGC CGCGCCGTGT CCACCGGGTC  
 60 12701 ACCGGGCCGG ACCGCGTCCG CACGGCGCCG CGCGGCGCCG TCGGGGGCGG

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5 12751 GGGCGGATCG CGGCGGTACG GGTTCGCGGG CGGTGTCCGC GGCGGTGCGC  
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12851 CCCGGTGGCC GTGTCCGCGG TGGCCGTGCC GGCAGGGGCG TCGCCGATGG  
10 12901 TCCGGCACAC CTCGTCCATC CGGTGCTTCA GATAGAAGTG ACCGCCGGCG  
12951 AAGGTGTGCA GGGCGAAGGG GCCCGTGGTC AGCTCCCGCC AGGCCCTCGC  
13001 CTCCTCCAGC GGGACATCGG GATCACGGTC ACCGGTGAGC ACCGTGACCG  
15 13051 GACAGTCCAG CGCACCGCCG GGCACATACG CGTACGTGCC CGCCGCCCGG  
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13151 GAGGACGGCG TCCTCGGTGC CCTGAAGCGT GGCATCTCC GCGATCAGCG  
20 13201 CGTCGTTCGTC GAGGAGGTGG GCGACGTCCC GCCGGCGCAC CGTCGGCGCA  
13251 CGGCGGCCCCG ACACCAGCAG ATGGACGGGG GAGGCCTGCC CGGAACCGCG  
25 13301 CAGCCGGCGC GCGACCTCGA ACGCCACCGT GGCACCCATG CTGTGCCCCA  
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13401 TCCACCAGGC CCGATATGGA CGGGATGAAC GGCTCGTGCC GGCGGTCCTG  
30 13451 GCGGCCCGGG TACTGCACCG CCAGCGCCTC CACGGTCTCG TCCAGTCCGC  
13501 GTGCCAGGGC GGCGAAGGAG GTCGCGGCGC CACCGGCGTG CGGGAAGCAG  
35 13551 ACCAGACGCA GTTCCGGATC CCGCACCGGG CGGTAACGGC GGACCCACAG  
13601 ACCCTCGTCC GGGTGTCCGG CCGGCGACGG GGCTCCCGGA ACGGGTGGTG  
13651 CGGAAGGGGT GCTCACGGCG GATCCAGCTC CTCGCGGTCG GGGGGACCGC  
40 13701 TGTCGGGGAC GGCACGTCCG GTGCGGACGT CGGGTACGGG CGTCGGGGCG  
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45 13801 GCGGCCCTTCT TCAGCGGTTT CCACCACGCG CGGTTCTCCG CGTACCAGCG  
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14001 GAGCAGCCGC TTCGTCAGCT CCCGGTTGGT CAGCTCCGTC CCGCCACCGA  
55 14051 TGTGGTAGAC CTCGCCCCGG CGCCCGCGGG TCGCCACCAG GCTGATCCCG  
14101 CGGCAGTGGT CGTCCACGTG CAGCCAGTCC CGGCTGTTGC CGCCGTCGCT  
14151 GTACAGCGGC ACCGTCAGAC CGTCCAACAG GTTCGTGGCG AAGAGCGGGA  
60 14201 CGACCTTCTC GGGGTGCTGG TACGGGCCGT AGTTGTTGGA GCACCGGGTG

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14251 ACGACGACCG GCAGGCCGTA CGTCCGGTGG TAGGCCAGCG CCAGGAGGTC  
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5 14351 CCTCGCGCCA CGACCCCTCG GCGATCGAGC CGTACACCTC GTCCGTGGAG  
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14451 TTGCGTCCCC CGTACGTTCG TCTCGACGAA CGCCGACGCG TCGGCGATGG  
10 14501 AGCGGTCCAC GTGCGACTCC GCCGGAAGT GGACCACGAC GTCCGCCCCC  
14551 CGCACGACCC GGGACATCAC CTCCGCGTCC CGGATGTCGG CGTGCACGAA  
15 14601 CTCCAGCGAC GGATGGTCCG CGACCGGGTC CAGGTTGGCG AGGTTCCCCG  
14651 CATAGGTCAG CTTGTGCGAC ACCACCGTCC GCGCCCCGCG CAGGTCCGGA  
20 14701 TACGCCCCGG CCAGCAGTTG TCTGACGAAG TGCGAGCCGA TGAAGCCCCG  
14751 ACCTCCGGTG ACCAGCAGCC GCATGGGAGC ACAGACCTTT CTTCCAGGGA  
14801 CGGGAAACGG GGAGGCGGAC GGGGACGGAG GCGAGGGCGG TGGCTATGCG  
25 14851 GCCGGTCCGG ACATGAGGGT CTCCGCCACG TCCATCAAGT ACCGGCCGTA  
14901 GCTGGAGCTC TCGAGTTCAC GGCCGAGCTC GTGGCACTGC CGCGCGCTGA  
14951 TGTACCCCAT CCGCAGGGCG ATCTCCTCGA CGCAGGAGAT CCGCACGCCC  
30 15001 TGCCGCTGCT CCAGGAGCTG GACGTACTGC CCCGCTTGCA GCAGCGAGCT  
15051 GTGCGTGCCC ATGTCCAGCC AGGCGAACCC GCGCCCCAGT TCCGTCATAC  
35 15101 GGGCGCGGCC CTGCTCCAGG TACACCTTGT TGACGTCGGT GATCTCCAGC  
15151 TCGCCCCGCG GCGACGGTGT CAGCCGCCGG GCGATGTCCA CCACGCCGTT  
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15251 GCTTCTCCTC CAGGGACACC AGCCGGCCTT CCGCGTCGAC CTCGCCGACG  
15301 CCGTAGCGCC GGGGGTCTTT CACCGGGTAG CCGAACAGCT CGCAGCCGTC  
45 15351 CAGCCGCGCC GCGGTGGAGG CCAGCACGGA GGAGAACCCC GGACCGTGGA  
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50 15451 TCGCCGATGA GGAACGCCTC GGCGATGCCC CGGGGCTCCT CCTGCTCGGC  
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15551 ACATCTCCAA GTGCGTCTTC GACGTGATGA TCTGGATGTC CCGGATCCCC  
55 15601 GCCAGCATGA GCACCGACAG CGGGTAGTAG ATCATGGGCT TGTCGTAGAC  
15651 CGGCAGCAAC TGCTTGGACA GTGCCCCGGT CAGGGGGCGC AGGCGCGTGC  
15701 CGCTGCCGCC CGCCAGGATG ATGCCCTTCA TGGGCCGCCG GTCCGCCGTC  
60 15751 GTCTTCGTCA T

**Figure 9**

|    |       |            |             |             |            |             |
|----|-------|------------|-------------|-------------|------------|-------------|
| 5  | 59800 |            |             |             |            | G           |
|    | 59801 | TGAGCCCCGC | ACCCGCCACC  | GAGGACCCGG  | CCGCCGCCGG | GCGCCGCCCTG |
|    | 59851 | CAACTGACCC | GCGCAGCCCA  | GTGGTTTCGCG | GGAACCCAGG | ACGACCCGTA  |
| 10 | 59901 | CGCGCTCGTC | CTGCGCGCCG  | AGGCCACCGA  | CCCGGCCCCG | TACGAGGAGC  |
|    | 59951 | GGATCCGGGC | CCACGGGGCCG | CTCTTCCGCA  | GCGACCTGCT | CGACACCTGG  |
| 15 | 60001 | GTCACGGCGA | GCAGGGCCGT  | CGCCGACGAA  | GTGATCACCT | CACCCGCCTT  |
|    | 60051 | CGACGGGCTC | ACGGCCGACG  | GGCGGCGCCC  | CGGCGCGCGG | GAAGTGCCGC  |
|    | 60101 | TGTCCGGCAC | CGCGCTCGAC  | GCGGACCGCG  | CCACATGCGC | ACGGTTCGGG  |
| 20 | 60151 | GCCCTCACCG | CCTGGGGCGG  | GCCGCTGCTG  | CCGGCGCCGC | ACGAGCGGGC  |
|    | 60201 | GCTGCGCGAG | TCCGCCGAAC  | GGCGGGCCCA  | CACACTCCTC | GACGGGGCGG  |
| 25 | 60251 | AGGCCGCCCT | GGCCGCCGAC  | GGCACCGTCG  | ACCTCGTCGA | CGCGTACGCC  |
|    | 60301 | CGCAGGCTCC | CCGCGCTGGT  | CCTCCGCGAA  | CAGCTCGGCG | TGCCGGAGGA  |
|    | 60351 | GGCGGCGACC | GCCTTCGAGG  | ACGCGCTGGC  | CGGCTGCCGC | CGCACCCCTGG |
| 30 | 60401 | ACGGCGCCCT | GTGCCCCGAA  | CTCCTCCCGG  | ACGCCGTGGC | GGGGGTGCGC  |
|    | 60451 | GCGGAAGCCG | CGCTGACCGC  | CGTGCTGGCC  | TCCGCCCTGC | GCGGGACTCC  |
| 35 | 60501 | GGCCGGCCGG | GCCCCGACG   | CCGTGCGCCG  | CGCCCGCACC | CTGGCCGTG   |
|    | 60551 | CGGCCGCCGA | GCCCCGAGCC  | ACCCTCGTCG  | GCAACGCCGT | ACAGGAGCTG  |
|    | 60601 | CTGGCGCGTC | CCGCGCAGTG  | GGCGGAGCTC  | GTACGCGACC | CGCGCCTCGC  |
| 40 | 60651 | GGCCGCCGCG | GTGACCGAAA  | CGTGCGTGT   | CGCCCCGCC  | GTCCGCCTGG  |
|    | 60701 | AGCGGCGGGT | CGCCCGCGAG  | GACACGGACA  | TCGCCGGGCA | GCGCCTCCCC  |
| 45 | 60751 | GCCGGGGGGA | GCGTCGTGAT  | CCTCGTCGCC  | GCCGTCAACC | GCGCGCCCGT  |
|    | 60801 | ATCCGCGGGA | AGCGACGCCT  | CCACCACCGT  | CCCGCACGCC | GGCGGCCGGC  |
|    | 60851 | CCCGTACCTC | CGCCCCCTCC  | GTCCCCTCAG  | CCCCCTTCGA | CCTCACACGG  |
| 50 | 60901 | CCCGTGGCCG | CGCCCGGGCC  | GTTCGGGCTC  | CCCGGCGACC | TGCACTTCGG  |
|    | 60951 | CCTCGGCGGG | CCCCTGGTCG  | GAACGGTCGC  | CGAAGCCGCG | CTCGGTGCGC  |
| 55 | 61001 | TGGCCGCACG | GCTCCCCGGT  | CTGCGCGCCG  | CCGGGCCGGC | CGTGCGGGCG  |
|    | 61051 | CGCCGCTCAC | CGGTGCTGCA  | CGGACACGCC  | CGCCTCCCCG | TCGCCGTGCG  |
|    | 61101 | CCGGACGGCC | CGTGACCTGC  | CCGCCACCGC  | ACCGCGGAAC | TGAGGAGGGA  |
| 60 | 61151 | GTGCCCCGAT | GCGTATCCTG  | CTGACGTCGT  | TCGCGCACAA | CACGCACTAC  |

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5 61201 TACAACCTGG TCCCCCTCGG CTGGGCGCTG CGCGCCGCCG GGCACGACGT  
61251 ACGGGTCGCC AGCCAGCCCT CGCTGACCGG CACCATCACC GGCTCCGGGC  
61301 TGACCGCCGT CCCCCTGGGC GACGACACGG CCATCGTCGA GCTGATCACC  
61351 GAGATCGGCG ACGACCTCGT CCTCTACCAG CAGGGCATGG ACTTCGTGGA  
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61451 TCATGTCGGC CATGTGCTTC TCGCCGCTGA ACGGCGACAG CACCATCGAC  
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20 61651 TTCACCCGGC TGCTCGCCGA GCGCCCCGTC GAACAGCGCG AGGACCCGGT  
61701 CGGCGAATGG CTCACGTGGA CGCTGGAGCG CCACGGCCTC GCCGCCGACG  
25 61751 CGGACACGAT CGAGGAAGTG TTCGCCGGGC AGTGGACGAT CGACCCAGC  
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61851 CGTGCCGTAC AACGGCGCCT CCGTCGTCCC CGCCTGGCTC TCCGAGCCGC  
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61951 TACGGCACGG ACGGCGTCCC GTTCCACGAA CTGCTGGCCG GACTGGCCGA  
35 62001 CGTGGACGCC GAGATCGTCG CCACCCTCGA CGCGGGGCAG CTCCCGGACG  
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62201 TCTGGGACGC GCCGCTGAAG GCGACCAAC TCGCCGAGGC GGGCGCCGGG  
62251 ATCGCCCTGG ACCCCGGGGA ACTGGGCGTG GACACCCTGC GCGGCGCCGT  
45 62301 CGTGCGGGTG CTGGAGAGCC GCGAGATGGC CGTGGCGGCG CGTCGCCTCG  
62351 CCGACGAGAT GCTCGCCGCC CCCACCCCGG CCGCGCTCGT CCCCCGCCTC  
50 62401 GAACGCCTCA CCGCCGCGCA CCGCCGCGCC TGATCCCGCC AAGGAGCCCC  
62451 CATGAACCTC GAATACAGCG GCGACATCGC CCGGTTGTAC GACCTGGTCC  
62501 ACCAGGAAA GGGCAAGGAC TACCGGGCGG AGGCCGAGGA GCTGGCCGCG  
55 62551 CTTGTCACCC AGCGCCGCCC CGGGGCCCGC TCCCTCCTCG ACGTGGCCTG  
62601 CGGAACGGGG ATGCACCTGC GGCACCTCGG CGACCTCTTC GAGGAGGTGG  
60 62651 CCGGGGTGGA GATGTCCCC GACATGCTGG CCATCGCGCA GCGGCGCAAC

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62701 CCGGAGGCCG GCATCCACCG GGGGGACATG CGGGACTTCG CCCTCGGCCG  
62751 CCGCTTCGAC GCCGTGATCT GCATGTTTCTG TTCCATCGGG CACATGCGCG  
5 62801 ACCAGCGGGA ACTGGACGCG GCGATCGGCC GTTTCGCCGC GCACCTGCCG  
62851 TCCGGCGGGG TCGTGATCGT CGATCCCTGG TGGTCCCCGG AGACGTTTAC  
10 62901 ACCGGGGTAC GTCGGCGCGA GCCTCGTCTG GGCCGAGGGC CGCACCATCG  
62951 CGCGCTTCTC CCACTCCGCG CTCGAGGACG GCGCGACCCG GATCGATGTG  
63001 GACTACCTCG TCGGCGTGCC GGGGGAGGGG GTGCGGCACT TGAAGGAGAC  
15 63051 CCATCGGATC ACGCTTTTCTG GGCCTGCGCA GTACGAGGCG GCCTTCACCG  
63101 CGGCGGGGAT GTCCGTCGAG TACCTCCCGC ACGCCGCCAC CGACCGCGGA  
20 63151 CTCTTCGTCG GCGTCCAGGC CTGA

25

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**Figure 10**

1 MKGIILAGGS GTRLRPLTGA LSKQLLPVYD KPMIYYPLSV LMLAGIRDIQ  
51 IITSKTHLEM FRSL LGDGSR IGISVGYAEQ EEPRGIAEAF LIGEEHIGDD  
101 PVALILGDNV FHGPGFSSVL ASTAARLDGC ELFGYPVKDP RRYGVGEVDA  
151 EGRLVSLEEK PEKPRSHLAV TGLYFYDNGV VDIARRLTPS PRGELEITDV  
201 NKVYLEQGRA RMTELGRGFA WLDMGTHSSL LQAGQYVQLL EQRQGVRI SC  
251 VEEIALRMGY ISARQCHEL G RELESSSYGR YLMDVAETLM SG PAA



**Figure 11**

1 MRLLVTTGGAG FIGSHFVRQL LAGAYPDLAG ARTVVVDKLT YAGNLANLDP  
51 VADHPSLEFV HADIRDAEVM SRVVRGADV VHFHAAESHVD RSIADASAFV  
101 ETNVRGTQVL LQAAVEAGAG RFVHVSTDEV YGSIAEGSWR EEQPLAPNSP  
151 YAASKAASDL LALAYHRTYG LPVVVTRCSN NYGPYQHPEK VVPLFATNLL  
201 DGLTVPLYSD GGNSRDWLHV DDHCRGISLV ATRGRPGEVY HIGGGTELTN  
251 RELTKRLLGL CGADASSVRH VADRPBGHDLR YALDIGKITG ELGYAPRTDF  
301 TTGLADTVRW YAENRAWWEP LKKAQEARR TD

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**Figure 12**

5  
1 VSTPSAPPVP GAPSPAGHPD EGLWVRRYRP VRDPELRLVC FPHAGGAATS  
51 FAALARGLDE TVEALAVQYP GRQDRRHEFF IPSISGLVDQ VVPEILRWAD  
101 RPLALFGHSM GATVAFEVAR RLRGSGQASP VHLLVSGRRA PTVRRRDVAH  
10 151 LLDDDALIAE IATLQGTEDA VLQDEELLRL ALPAIRNDYR AAGTYAYVPG  
201 GALDCPVTVL TGDRDPDVPL EEARAWRELT TGPFALHTFA GGHFYLNDRM  
251 DEVCRTIGDA LAGTATADTA TGTVPPTAA DTSTGPVPPR TAADTAREPV  
15 301 PPRSAPAPHG AARRRADAVR PGDPVDTARR VLVSARTADS AVTPFDGISG  
351 WLAERLRAGR FDVSRVPFAE LRGWSFHPGT GNLHHASGRF FSVEGLHVRT  
20 401 DRLPERGWTQ PIIVQPEVGL LGIVAREIDG VLHFLMQAKM EPGNVNVLQV  
451 SPTVQATRSN FTGVHRGRDI RYLDLFMGPR RARVLVDSIQ SEQADWFLAK  
501 RNRNMIVELA ADDDLDIGED FRWLTGQLR RLLMLDNVNN MDARSILACL  
25 551 PTADADASAP SPVLSFFGS PGAARHTTAE VLTWFTGVRA LRELQNRVP  
601 LDTVTDGWY RTPHEIAHES GRHFRVMAAE VSASSREVTS WTQPLIEPRL  
30 651 PGLMALLVKS VDGVLHALVR ARVDVGHLNV AELAPTVQCR PQEHTGPRGL  
701 PGPPYLEDVL SAPPQDVRYD AVQSEEGGRF FHAQNRYVIV EVPHDFPEDA  
35 751 PDDFAWLSLG QLTGLLAHGN YLNIELRTL V ACAHTLY  
40

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**Figure 13**

5           1   MVNDPMFRGS GSGSVVVLGG AGYVGRHVCA AFAARGRDVV VVGRRPPEEP  
          51   MPYRCVTLDL AGTDPAALAA ALDAERPDTI VNSVGSIWGR TDEQMWSATA  
         101   VPTLRLLEAL ALMSARFRLV HLGSVLEYGP VTPGGSVGAD AVPRPDYAYG  
0           151   RSKLAASEAV LRGTSGGWVD GVVLRVSNVS GPGTPRISLL GQVAERLLAA  
          201   AGTGAEAVVE LSRLRAHRDY VDVRDVADAV VAAARAPAVP VAVGIGRGEA  
5           251   VAVRDLVGLF IEASGIPARV VERPAPGRAP GHREDWLRVD TGAARALLGW  
          301   APRRSLRESV RDCWHDLVRA HRLPTTPSKH SGG

20

**Figure 14**

5           1   VTTYVWDYLA EYQNERADLL DAVETVFASG QLVLGPSVDG FEKEFADYHG  
          51   LRHCGGVDNG TNAVKLGLQA LGVGPGEDEVV TVSNTAAPT VVAIDGTGATP  
10       101   VFVDVRAEDH LMDTDQVADV ITPRTKALLP VHLYGQCVD M APLRALAEQH  
         151   GLVVLEDCAQ AHGARHHGEL AGTLGDAAAF SFYPTKVLGA YGDGGAVLTD  
         201   DADVDRALRR LRYYG MEDVY YVVQTPGHNS RLDEVQAEIL RRKLTRLDRY  
15       251   IEGRRAVARR YAEGLANLTG PGGLVLPSVT EGNDHVYYVY VVRHPRRDDI  
         301   IEALKSYGIS LNISYPWPVH TMTGFAHLGY AKGSLPVTER LADEIFSLPM  
         351   YPGLAPDVQD KVIAALHEVL ATL  
20

25

**Figure 15**

5           1   VSPAPATEDP AAAGRRLQLT RAAQWFAGTQ DDPYALVLRA EATDPAPYEE  
          51   RIRAHGPLFR SDLLDTWVTA SRAVADEVIT SPAFDGLTAD GRRPGARELP  
10       101   LSGTALDADR ATCARFGALT AWGGPLLAP HERALRESAE RRAHTLLDGA  
         151   EAALAADGTV DLVDAYARRL PALVLREQLG VP EEAATAFE DALAGCRRTL  
         201   DGALCPQLLP DAVAGVRAEA ALTAVLASAL RGTPAGRAPD AVAAARTLAV  
15       251   AAAEPAATLV GNAVQELLAR PAQWAEIVRD PRLAAAVTE TLRVAPPVRL  
         301   ERRVARETD IAGQRLPAGG SVVILVAVN RAPVSAGSDA STTVPHAGGR  
         351   PRTSAPSVPS APFDLTRPVA APGPFGPLPGD LHFRLGGPLV GTVAEAAALGA  
20       401   LAARLPGLRA AGPAVRRRRS PVLHG HARLP VAVARTARDL PATAPRN

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**Figure 16**

5  
1 MRILLTSFAH NTHYYNLVPL GWALRAAGHD VRVASQPSLT GTITGSGSLTA  
51 VPVGDDTAIV ELITEIGDDL VLYQQGMDFV DTRDEPLSWE HALGQQTIMS  
101 AMCFSPNLGD STIDDMVALA RSWKPDVLVW EPFTYAGPVA AHACGAAHAR  
10 151 LLWGPDVVLN ARRQFTRLLA ERPVEQREDP VGEWLTWTLE RHGLAADADT  
201 IEELFAGQWT IDPSAGSLRL PVDGEVVPMP FVPYNGASVV PAWLSEPPAR  
15 251 PRVCVTLGVS TRETYGTDGV PFHELLAGLA DVDAEIVATL DAGQLPDAAG  
301 LPGNVRVVDF VPLDALLPSC AAIVHHGGAG TCFTATVHGV PQIVVASLWD  
351 APLKAHQLAE AGAGIALDPG ELGVDTLRGA VVRVLESREM AVAARRLADE  
20 401 MLAAPTPAAL VPRLERLTAA HRRA

25

**Figure 17**

5           1   MNLEYSGDIA RLYDLVHQK GKDYRAEAE LAALVTQRRP GARSLLDVAC  
          51   GTGMHLRHLG DLFEEVAGVE MSPDMLAIAQ RRNPEAGIHR GDMRDFALGR  
10       101   RFDVICMFS SIGHMRDQRE LDAAIGRFAA HLPSSGGVVIV DPWWFPETFT  
         151   PGYVGASLVE AEGRTIARFS HSALEDGATR IDVDYLVGVP GEGVRHLKET  
         201   HRITLFGRAQ YEAAFTAAGM SVEYLPHAAT DRGLFVGVA

15